



## Glucohexaose-induced protein phosphatase 2C regulates cell redox status of cucumber seedling

QM CHEN<sup>1</sup>, Y YU<sup>2</sup>, CM LIN<sup>2</sup>, N CUI<sup>1,3\*</sup>, JY ZHAO<sup>4</sup>, TF SONG<sup>3</sup> and HY FAN<sup>1,2\*</sup>

<sup>1</sup>College of Horticulture, Shenyang Agricultural University, Shenyang 110866, People's Republic of China

<sup>2</sup>College of Bioscience and Biotechnology, Shenyang Agricultural University, Shenyang 110866, People's Republic of China

<sup>3</sup>Key Laboratory of Protected Horticulture of Ministry of Education, Shenyang Agricultural University, Shenyang 110866, People's Republic of China

<sup>4</sup>Liaoning Academy of Agricultural Sciences, Shenyang 110866, People's Republic of China

\*Corresponding authors (Email, syaua@163.com, hyfan74@163.com)

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Protein Phosphatase 2C (PP2C) is an important phosphatase-like protein in eukaryotic organisms that can negatively regulate protein kinase cascade abscisic acid (ABA) signal system through phosphorylation and carry out vital roles in various cell processes. The previous study indicated that the accumulation of reactive oxygen species (ROS) is a part of mechanism of glucohexaose-induced resistance in cucumber cotyledons, and *CsPP2C80s* might play a crucial role in processes related to ROS produce and signal transduction. To identify the mechanism of *CsPP2C80s* involved in glucohexaose and ABA signaling regulating cell redox status, the effects of glucohexaose and ROS inhibitor pretreatment on endogenous ABA content and ABA signaling genes expression levels of cucumber seedlings were analysed. These results suggest that cucumber *CsPP2C80s* are involved in ROS accumulation and ABA signal transduction pathway induced by glucohexaose, *CsPP2C80s* play a positive regulatory role in process of ABA combined with ABA receptors (PYLs) to activate SNF1-related protein kinases 2 (SnRK2s) and regulate NADPH oxidase to produce extracellular hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>), providing unequivocal molecular evidence of PP2C-mediated ABA response mechanisms functioning in cell redox status induced by glucohexaose.

**Keywords.** ABA; glucohexaose; PP2C; qRT-PCR; ROS inhibitor

### 1. Introduction

In the process of growth and development, the plants form the ability to resist pests and diseases. Induced resistance (IR) is a special acquired immunity after plant is stimulated by biological or non-biological factors. Compounds such as oligosaccharides and proteins can induce the plant to produce defensive reactions (Strobel *et al.* 1996; Thuerig *et al.* 2006; Saravanakumar *et al.* 2007; Huang *et al.* 2012). Oligonucleotides are the elicitors that are earliest studied (Sharp *et al.* 1984) Glucohexaose, synthesized by Research Center for Eco-Environmental Science, Chinese Academy of Science as an oligosaccharide. Uronic acid oligosaccharide of plant cell wall derives regulatory factors, which can stimulate the expression of defense genes in pathogen infection process, and enhances pp34 protein phosphorylation (Reymond *et al.* 1995). We found that cucumber resistance systems were stimulated and acquired defensive

capacity to *Pseudoperonospora cubensis* after glucohexaose incubation (Hao *et al.* 2013). These oligosaccharides induce plant defense systems as signaling molecules.

Protein Phosphatase 2C (PP2C) is evolutionary conserved from prokaryotes to eukaryotes and play a prominent role in various signaling pathways and plant development. In plants, PP2Cs are considered to be the largest protein phosphatase family as regulators of signal transduction pathways and involved in plant development. Studies have showed that protein dephosphorylation plays a crucial role in regulating signaling cascades in response to abscisic acid (ABA) and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) in guard cells (Schmidt *et al.* 1995; Mori and Muto 1997). PP2C is a direct target of reactive oxygen species (ROS) in ABA signaling (Meinhard and Grill 2001; Meinhard *et al.* 2002). The signal pathways most closely related to ROS accumulation includes mitogen-activated protein kinase (MAPK), ABA and Ca<sup>2+</sup> signal. ROS is participates in the process of plant growth,

development, hormonal signaling and responses to environmental stimuli in plants (Apel and Hirt 2004; Mittler et al. 2004; Kwak et al. 2006; Torres et al. 2006; Suzuki et al. 2011). Currently, the physiological and biochemical changes is associated with the outbreak of ROS, the production of plant hormone, the pathogenesis-related proteins and the defensive enzymes (Liu et al. 2004; Chisholm et al. 2006; Vos et al. 2013). Coincidentally, PP2C plays a critical role in these signals (Bertauche et al. 1996; Gaits et al. 1997; Yoshida et al. 2006). At present, six kinds of PP2C protein phosphatases have been found in plants, including ABI1, ABI2, HAB1, HAB2, AHG1 and PP2CA/AHG3. Genetic research has indicated that PP2Cs, ABI1 and ABI2 of Arabidopsis were as negative regulators participating in ABA signaling pathway (Armstrong et al. 1995; Sheen 1998; Gosti et al. 1999; Merlot et al. 2001). At present, a large number of *PP2C* genes have been cloned in plants, and the studies focus on their roles in different signaling pathways, for example, the biological function of ABI1 and ABI2 has been understood more clearly (Leung et al. 1994). Phosphorylation of PP2C protein plays an important role in the ABA signaling pathway, and some PP2C protein kinases are isolated and described as ABA signaling factors (Hirayama and Shinozaki 2010). *AtPP2C* participates in stomatal closure and plays a negative regulatory role in ABA signaling (Tahtiharju and Palva 2001). *MpABI1* is a negative regulator of ABA signaling, which provide molecular evidence of PP2C-mediated ABA response mechanism function (Tougan et al. 2010). Screening mutants and yeast two-hybrid methods were used to determine a new ABA receptor PYR / PYL / RCAR protein in Arabidopsis (Park et al. 2009; Ma et al. 2009). The increase of residues in the ABA/PYL10 complex may enhance the interactions between PP2C and PYL10, leading to an increase in PP2C phosphatase inhibition by PYL10 (Li et al. 2015). In normal growing conditions, dephosphorylation of clade A PP2C makes SnRK2 inactivation and ABA signal keeping silent. Once the environmental conditions or developmental signals stimulate plants, ABA will be induced and combine with PYR / PYL / RCAR interacting with the clade A of PP2C, inhibiting the activity of SnRK2. As SnRK2 phosphorylate downstream transcription factors or membrane protein factors, ABA signal pathway is open (Raghavendra et al. 2010). ABA can induce ROS accumulation and stomatal closure but NADPH oxidase double mutant *atrbohD/F* cannot (Kwak et al. 2003). ABA can elevate H<sub>2</sub>O<sub>2</sub> content in corn embryo and seedlings (Guan et al. 2000; Jiang and Zhang 2002; Pei et al. 2000; Zhang et al. 2001). The activities of ABI1 and ABI2 are suppressed by H<sub>2</sub>O<sub>2</sub> in Arabidopsis (Meinhard and Grill 2001, 2002).

Our previous study found that the content of O<sup>2-</sup> and H<sub>2</sub>O<sub>2</sub> dramatically increased after 5h by glucohexaose treatment in cucumber, and then O<sup>2-</sup> gradually reduced while H<sub>2</sub>O<sub>2</sub> increased sustainable to 10h after treatment, however,

the accumulation of ROS inhibited by diphenyleneiodonium chloride (DPI, an inhibitor of NADPH oxidase) and dimethylthiourea (DMTU, a ROS scavenger) pretreatment. Two-dimensional electrophoresis (2-DE) coupled with mass spectrometry analysis revealed that AtPP2C 80 (15240071) related to the outbreak of ROS activated in the control of redox state by glucohexaose. Multiple sequence alignment analysis indicated that two PP2C80 related proteins (Cucsa201270 and Cucsa342170) were identity with AtPP2C 80 in cucumber. The results indicated that PP2C was a ROS-related and glucohexaose-induced protein, which might have important function either in ROS accumulation and signal transduction (Hao et al. 2014).

## 2. Materials and methods

### 2.1 Materials and experimental design

Cucumber seeds (Jinyan No.4) were soaked in distilled water for 2 h, sterilized with 75 % ethanol for 60 s, 2.5 % NaClO for 13 min and then washing at least three times. The seeds were placed on soaked gauze and germinate at 25–28°C. Until the cotyledons expanded, the seedlings were used for subsequent experiments.

To investigate the effect of glucohexaose in the process of *CsPP2C80s* expression and ABA content changes, a part of the seedlings were sprayed with 50 µg.mL<sup>-1</sup> glucohexaose and deionized water was used to spray control seedlings. Seedlings were sampled at 0, 1, 5, 9, 10 and 14 h after glucohexaose treatment, stored at -80°C.

To investigate the effect of DPI (an inhibitor of NADPH oxidase) and DMTU in the process of the oxidative burst, the materials were divided into six groups. The first (control plants) and second groups of materials were sprayed with deionized water and 50 µg.mL<sup>-1</sup> glucohexaose respectively after incubating with deionized water in advance for 4 h. The third and fourth groups of materials were sprayed with 50 µg.mL<sup>-1</sup> glucohexaose after incubating with 100µM DPI and 5mM DMTU for 4 h respectively. The fifth and sixth groups of materials were sprayed with deionized water after incubating with 100µM DPI and 5mM DMTU for 4 h respectively. Seedlings were harvested at 5 h after being sprayed by glucohexaose or deionized water, and then stored at -80°C.

### 2.2 To determine ABA concentrations

Approximately 0.5g samples were collected into liquid nitrogen and homogenized in 80% chilled methanol. The supernatant was collected after centrifugation, purified through a C18 cartridge column and eluted with 80% methanol. The ABA level was determined using the enzyme-

linked immunosorbent assay (ELISA) test kit according to the instructions.

### 2.3 Quantitative real-time PCR (qRT-PCR) expression analysis

Total RNA was isolated from different samples of cucumber seedlings sprayed by glucosylated, glucosylated with DPI pretreatment, glucosylated with DMTU pretreatment. The cDNA was generated using a QuantScript RT kit (TianGen). The TianGen SuperReal PreMix Plus (SYBR Green) PCR kit was used for qRT-PCR analysis. All primer sequences were showed in table 1.

Quantitative real-time PCR analysis was conducted using a Roche LightCycler 480. Relative quantification of the gene expression was calculated by the  $2^{-\Delta\Delta Ct}$  method. All experiments were based on three biological replicates.

## 3. Results

### 3.1 Changes of PP2C after the treatment of glucosylated

There are about 60 PP2C genes in cucumber. Our previous study showed that AtPP2C 80 was a glucosylated-induced protein, which might have function in ROS accumulation and signal transduction. Multiple sequence alignment analysis indicated that two CsPP2C80s are identity with AtPP2C

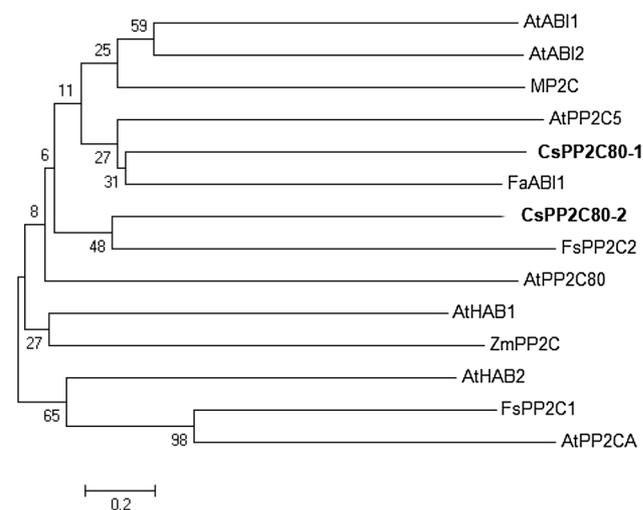
80 in cucumber. In order to detect the relationship between CsPP2C80s and genes involved in ABA signaling from other plants, nucleotide sequences from Arabidopsis (*ABI1*, *ABI2*, *HAB1*, *HAB2*, *AtPP2CA*, *AthPP2C5* and *AtPP2C80*), beeches (*FsPP2C1*, *FsPP2C2*), alfalfa (*MP2C*), corn (*ZmPP2C*), strawberries (*FaABI1*), and cucumber (*CsPP2C80-1*, *CsPP2C80-2*) were aligned using Molecular Evolutionary Genetics Analysis (MEGA) software. The phylogenetic tree indicated that *CsPP2C80-1* was the highest homology with strawberries *FaABI1* and *CsPP2C80-2* was the highest homology with beech *FsPP2C2* (figure 1).

In our previous study, to clarify the role and mechanism of ROS burst out in the resistance of cucumber induced by glucosylated, the differential proteomics method was used to study the oligodeoxynucleotides elicitor and the effect of NADPH oxidase inhibitor (DPI) and H<sub>2</sub>O<sub>2</sub> scavenger (DMTU) on the different expression of protein in cucumber cotyledons. Studies have shown that PP2C protein content is significantly upregulated after glucosylated induction, whereas DMTU and DPI pretreatment will inhibit this increase in some extent, and DMTU inhibitory effect is more obvious (Hao et al. 2014).

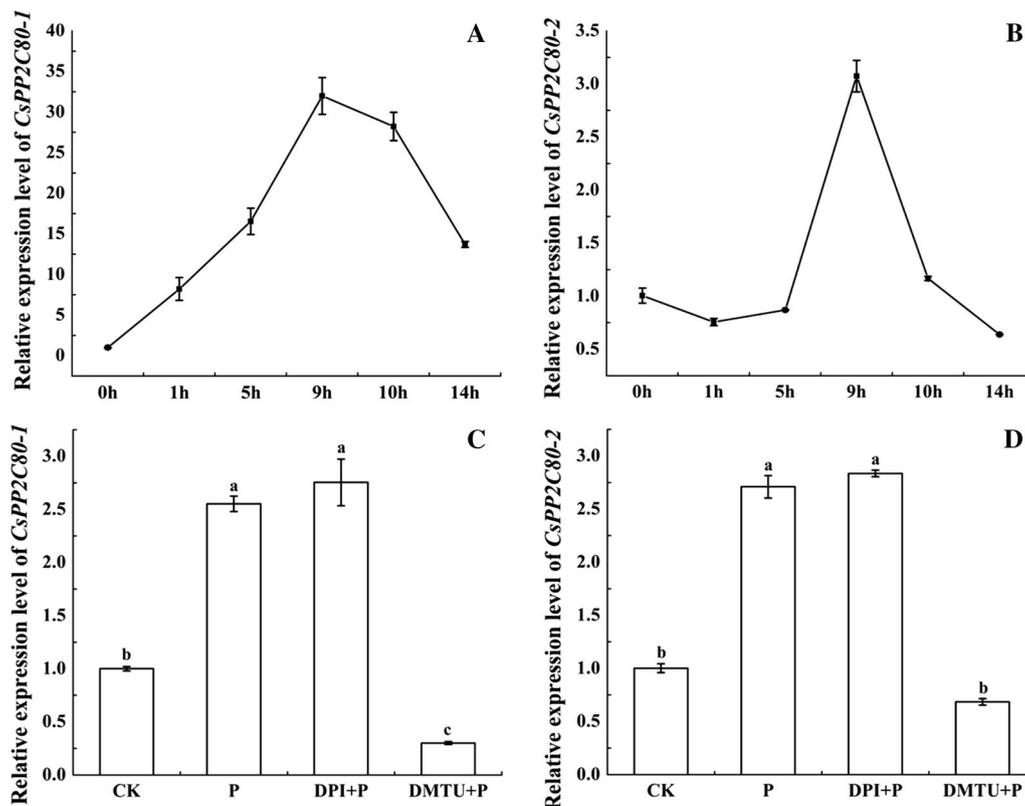
To indicate whether *CsPP2C80s* were involved in glucosylated-induced response, the mRNA expression pattern of *CsPP2C80s* under glucosylated-induced treatment was examined by qRT-PCR (figure 2A, B). The transcripts of *CsPP2C80s* were significantly induced in response to glucosylated treatment. The expression levels of *CsPP2C80s* were increased rapidly from 0 h to 9 h peaked at 9 h, and then decreased continuously.

**Table 1.** Primer sequences used for qRT-PCR

Gene name	Primer sequence (5' to 3')
<i>18S Rrna-F</i>	ATGATAACTCGACGGATCGC
<i>18S Rrna-R</i>	CTTGATGTGGTAGCCGT
<i>CsPP2C80-1-F</i>	ATGTAGTTGGCGTTGCGGATGGT
<i>CsPP2C80-1-R</i>	TAGCCGTAGTGCCGAGTGAGCT
<i>CsPP2C80-2-F</i>	TTTTCTATCCCTCCGTGTC
<i>CsPP2C80-2-R</i>	CCATTATTGTTAGGCTGCTC
<i>PYL1-F</i>	CTTTGTGGAAGCCTTGATT
<i>PYL1-R</i>	TATACCCTCCTGCCTGTCC
<i>PYL2-F</i>	CAGGCTTAGGAACTACTCT
<i>PYL2-R</i>	TAAATGACTCAACCACCAG
<i>PYL3-F</i>	GCTACACCGCCACTACTCCC
<i>PYL3-R</i>	GCAGACCTGACACCACCTCC
<i>SnRK2.1-F</i>	CGGCATACATAGCACCCAG
<i>SnRK2.1-R</i>	GCACCGACCAACATAACA
<i>SnRK2.2-F</i>	CAGAAATCAAGAAGCACCCA
<i>SnRK2.2-R</i>	CTCCAAGGCACAAACAAAGT
<i>Rboh F-F</i>	CCAGCACAGGACTACCAT
<i>Rboh F-R</i>	AGGAGCGTGACAATCTTT
<i>Rboh A1-F</i>	GGAGGAGTTTGTGGAGGTG
<i>Rboh A1-R</i>	CGTCGATATTGATTATAGTGGC
<i>Rboh A2-F</i>	GAGCCAGAACATACAGGGAC
<i>Rboh A2-R</i>	ATGGAGAATGACGCCAACTA



**Figure 1.** Phylogenetic tree analysis of different sources of plant PP2Cs. The tree was constructed using the neighbor-joining method provided in MEGA 4.0 software. Bootstrap values (1,000 replicates) were given below the branches.



**Figure 2.** Relative expression patterns of *CsPP2C80s* mRNA. (A and B) Treated with glucohexaose. (C and D) Treated with P, DPI+ P and DMTU+P respectively. Each sample was individually assayed in triplicate. CK: Control check. Sterile water treatment; P: Glucohexaose treatment 5 h; DPI+P/DMTU+P: DPI/DMTU pretreatment 4h and glucohexaose treatment 5h; DPI/DMTU: DPI/DMTU treatment 4 h. Lowercase letters:  $P < 0.05$ .

ROS ( $H_2O_2$  and  $O_2^{\cdot -}$ ) significant accumulation occurred at 5h after treat with glucohexaose. DMTU and DPI pretreatment suppressed the effect of glucohexaose (Hao *et al.* 2014). To evaluate whether *CsPP2C80s* expression were affected by ROS inhibitors, the levels of *CsPP2C80s* transcript in seedlings were studied by qRT-PCR analysis (figure 2C, D). Following DMTU pretreatment, the expression of *CsPP2C80s* decreased significantly compared to glucohexaose treatment. The inhibiting effect was not obvious after DPI treatment.

### 3.2 Alteration of ROX status induced by glucohexaose affected ABA levels and ABA-responsive gene transcripts

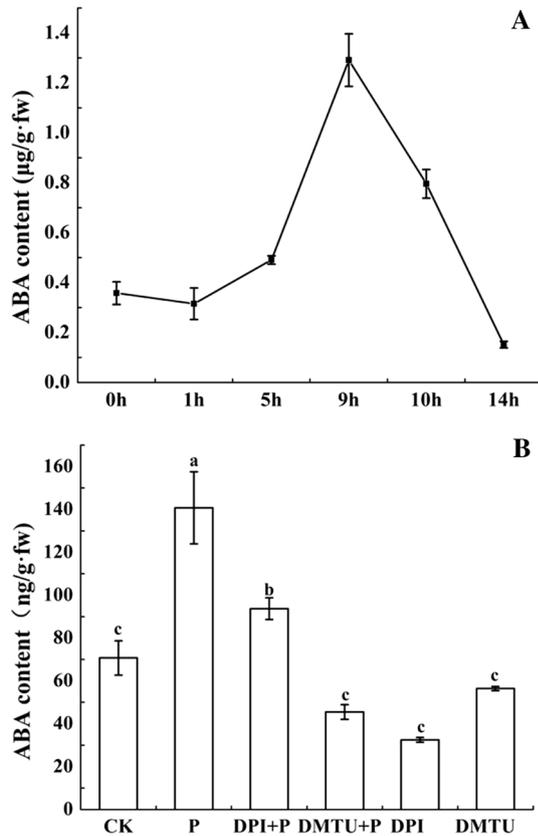
To confirm the mechanism of *CsPP2C80s* in the regulation of cucumber seedling redox status induced by glucohexaose, several inducing-related physiological parameters were measured, including ABA content and a set of ABA-responsive genes, such as *PYL*, *SnRK2*, *RbohA*.

The results showed that ABA content increased continuously from 0 h to 9 h after glucohexaose treatment, the content of ABA were extremely high at 9 h, and then

declined rapidly. ABA content returned to the control treatment level at 14 h (figure 3A). The exaltation of ABA was later than the accumulation of ROS after glucohexaose treatment. Meanwhile, the ABA content failed to accumulate after DPI and DMTU pretreatment (figure 3B).

Previous studies have shown that PYR/PYL/RCAR could combine with ABA directly, and different family member of PYR/PYL/RCAR selected different ABA steric configuration (Szostkirwicz *et al.* 2010). PYR/PYL/RCAR receptors could inhibit PP2C phosphatase activity through interaction with clade A of PP2C.

The qRT-PCR analysis indicated that the family members of ABA receptors were differentially expressed in response to various treatments. The expression patterns of *PYL1*, *PYL2*, and *PYL3* were significantly up-regulated and peaked at 10h, 9 h and 10 h after glucohexaose treatment, respectively (figure 4A, B, C). However, the expression levels of *PYL1*, *PYL2* and *PYL3* were all markedly down-regulated after DPI and DMTU pretreatment compared to glucohexaose treatment alone (figure 4D, E, F). Meanwhile, *PYL1* and *PYL3* expression level was obviously induced by glucohexaose treatment, but the effect of DPI and DMTU pretreatment on *PYL1* expression was more obvious.



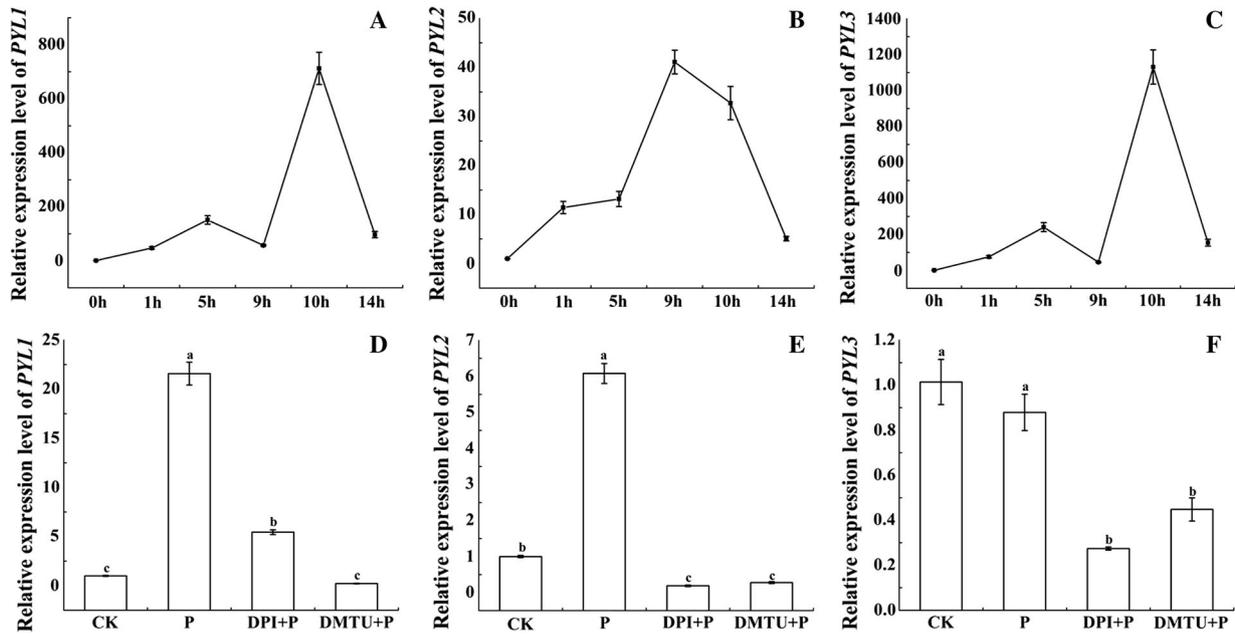
**Figure 3.** The content of endogenous ABA. **(A)** Treated with glucohexaose. **(B)** Treated with P, DPI +P, DMTU+P, DPI and DMTU respectively. Each sample was individually assayed in triplicate. CK: Control check. Sterile water treatment; P: Glucohexaose treatment 5 h; DPI+P/DMTU+P: DPI/DMTU pretreatment 4h and glucohexaose treatment 5h; DPI/DMTU: DPI/DMTU treatment 4 h. Lowercase letters:  $P < 0.05$ .

In plants, sucrose nonfermenting-1 (SNF1)-related protein kinases (SnRKs) involve in the stress responses and metabolic regulation (Halford and Hey, 2009; Hey *et al.* 2010). SnRKs can be subdivided into three sub-families: SnRK1, SnRK2, and SnRK3 (Halford, 2005). A key role for SnRK2 in ABA signaling pathway has been found with the identification of PYR/PYL/RCAR proteins as ABA receptors and involve in ABA signalling (Leung *et al.* 1997). ABA regulates the activity of SnRK2, which, in turn, activates ABA response element binding proteins (AREBPs) inducing gene expression (Coello *et al.* 2011). In this experiment, our qRT-PCR analysis indicated that *SnRK2.1* and *SnRK2.2* expression levels were induced by glucohexaose treatment, and the highest expression level were observed at 9h and 10h, respectively (figure 5A, B). However, the expression pattern of *SnRK2.1* and *SnRK2.2* were significantly inhibited by pretreatment with DPI and DMTU (figure 5C, D).

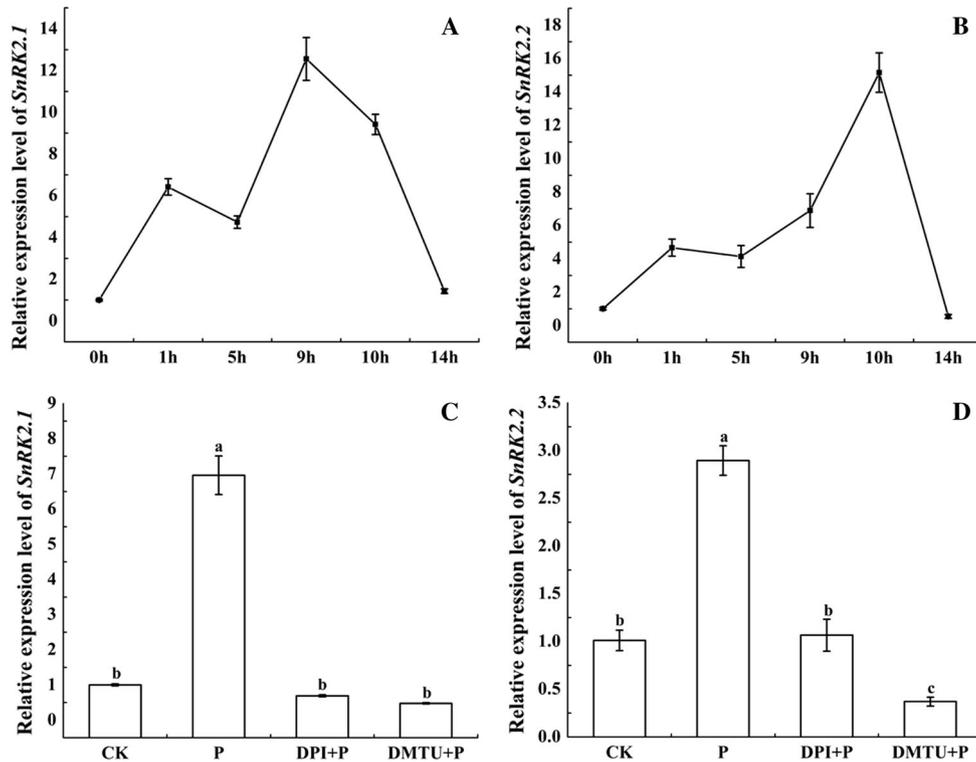
A key factor in the network of ROS produce is the special respiratory burst or NADPH oxidase (Torres and Dangel 2005). NADPH oxidases are the source of ROS produce in ABA signaling and other processes, such as plant cell growth and defense response (Torres *et al.* 2002; Foreman *et al.* 2003; Kwak *et al.* 2006). RbohA and RbohB are involved in  $H_2O_2$  accumulation and viral resistance in *Nicotiana benthamiana* (Yoshioka *et al.* 2003). RbohD and RbohF are required for ROS accumulation intermediates in plant defense response and participate in ROS-dependent ABA signaling (Torres *et al.* 2002; Foreman *et al.* 2003; Bright *et al.* 2006). In this experiment, the qRT-PCR analysis indicated that *RbohA1*, *RbohA2* and *RbohF* were induced in response to glucohexaose treatment. The transcript pattern of *RbohA1*, *RbohA2* and *RbohF* increased at early stage, decreased from 2 h to 9 h, and then increased again (figure 6A, B, C). The results suggested that glucohexaose treatment could induce *Rbohs* gene expression at early stage. The expression pattern of *RbohA1* and *RbohF* were inhibited by pretreatment with DPI and DMTU (figure 6D, F), but the expression of *RbohA2* was further up-regulated by pretreatment with DPI and DMTU (figure 6E).

#### 4. Discussion

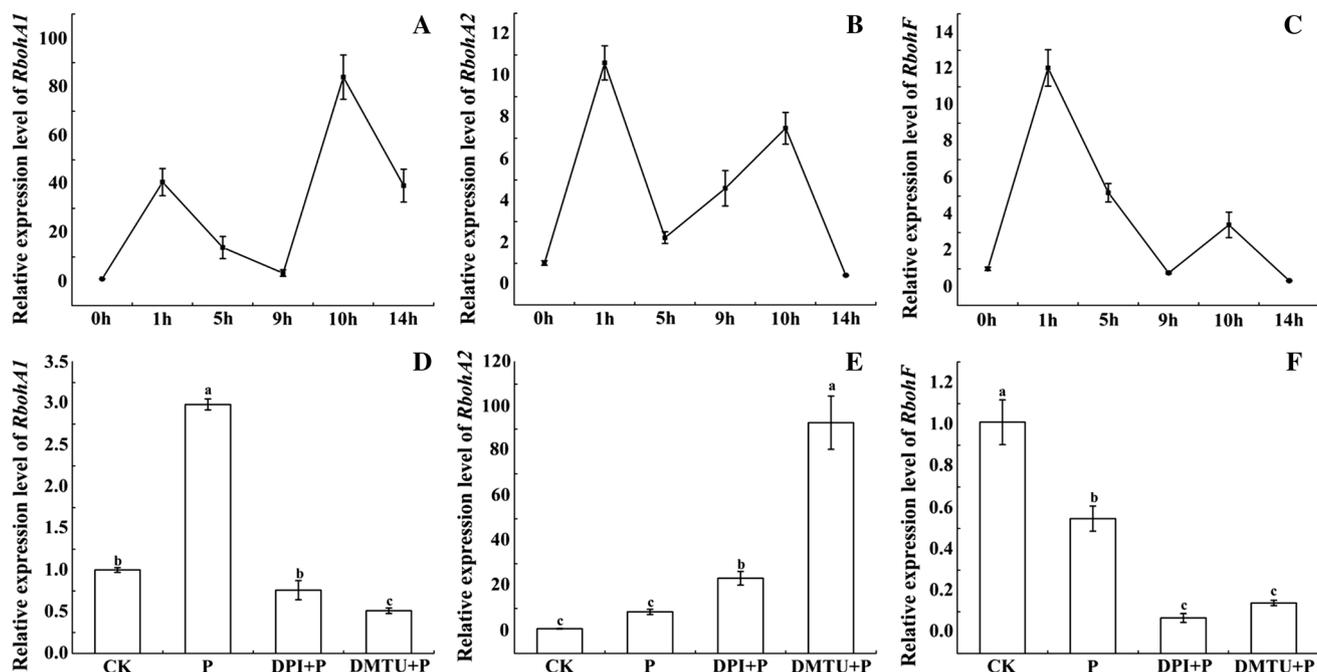
In agricultural production, how to prevent disease without pesticide residues has attracted more attention. Elicitors can protect crops from pest, disease or environmental stress. Researches show that elicitors can cause ROS accumulation rapidly and trigger defense response (Bradley *et al.* 1992; Svalheim and Robertsen 1993; Nürnberger *et al.* 1994; Auh and Murphy 1995). Glucohexaose is a synthetic oligosaccharide elicitor that can activate plants acquired resistance to *Pseudoperonospora cubensis* (Fan *et al.* 2003). Our previous study confirmed that the ROS accumulation was a part of the mechanisms of glucohexaose-induced resistance and PP2C might play a crucial role in processes related to ROS produce and signal transduction (Hao *et al.* 2014). We had no idea whether glucohexaose-induced resistance was related to ABA signaling, why PP2C accumulated after ROS content increased and whether *CsPP2C80s* were involved in ABA signaling pathway. Therefore, we sought to further investigate the possible link among ROS accumulation, PP2C, ABA signaling and glucohexaose-induced resistance. We reported that glucohexaose-induced resistance was related to ROS and ABA signaling, that *CsPP2C80s* played an important role in process of ABA combined with PYLs to activate SnRK2s and thereby regulated NADPH oxidase to produce extracellular  $H_2O_2$  in cucumber. These results provided important clues of the mechanism of glucohexaose-induced resistance. We found that the expression of *CsPP2C80s* was induced after glucohexaose treatment, and this increase would be inhibited by active oxygen inhibitors



**Figure 4.** Relative expression patterns of *PYLs* mRNA using the qRT-PCR method. (A) Relative expression pattern of *PYL1* mRNA after glucohexaose treatment; (B) *PYL2*; (C) *PYL3*; (D) Relative expression patterns of *PYL1* gene after P, DPI+ P and DMTU+P treatments, respectively; (E) *PYL2*; (F) *PYL3*. Each sample was individually assayed in triplicate. CK: Control check. Sterile water treatment; P: Glucohexaose treatment 5 h; DPI+P/DMTU+P: DPI/DMTU pretreatment 4h and glucohexaose treatment 5h. Lowercase letters:  $P < 0.05$ .



**Figure 5.** Relative expression patterns of *SnRK2s* mRNA using the qRT-PCR method. (A) *SnRK2.1* gene expression pattern after glucohexaose treatment; (B) *SnRK2.2*; (C) *SnRK2.1* gene expression patterns after P, DPI+ P and DMTU+P treatments, respectively; (D) *SnRK2.2*. Each sample was individually assayed in triplicate. CK: Control check. Sterile water treatment; P: Glucohexaose treatment 5 h; DPI+P/DMTU+P: DPI/DMTU pretreatment 4h and glucohexaose treatment 5h. Lowercase letters:  $P < 0.05$ .



**Figure 6.** Relative expression patterns of *Rbohs* mRNA using the qRT-PCR method. (A) *RbohA1* gene expression pattern after glucosaxose treatment; (B) *RbohA2*; (C) *RbohF*; (D) *RbohA1* gene expression patterns after P, DPI+ P and DMTU+P treatments, respectively; (E) *RbohA2*; (F) *RbohF*. Each sample was individually assayed in triplicate. CK: Control check. Sterile water treatment; P: Glucosaxose treatment 5 h; DPI+P/DMTU+P: DPI/DMTU pretreatment 4h and glucosaxose treatment 5h. Lowercase letters:  $P < 0.05$ .

DMTU and DPI pretreatment, which indicated that CsPP2C80s might participate in the accumulation of ROS by glucosaxose regulation in cucumber seedlings.

ABA signaling pathway includes PYR/PYL/RCAR, PP2C, and SnRK2. PP2Cs exclusive interact with ABA receptors and SnRK2s (Umezawa *et al.* 2009; Ma *et al.* 2009; Park *et al.* 2009). The diversity of PP2C in plants shows the diversity of signal transduction mechanisms in different tissues and organs. PP2C homolog gene *PeHAB1* is a new negative regulator of ABA signaling in poplar (Chen *et al.* 2015). Previous reports found that clade A of PP2C inhibited the release of signaling triggered by ABA (Fuchs *et al.* 2013; Tougane *et al.* 2010). Beech *FsPP2C1* is reported to be a positive regulator in ABA signaling pathway, and involved in the synthesis and metabolism of gibberellic acid (GA) (Reyes *et al.* 2006). *FaABI1* had been detected to be a negative regulator of strawberry fruit ripening, and it was suggested that the ABA-FaPYR1-FaABI1-FaSnRK2 signalling pathway might be an important mechanism in non-climacteric fruit (Jia *et al.* 2013). In this study, the phylogenetic tree indicated that *CsPP2C80-1* was the highest homology with strawberries *FaABI1* and *CsPP2C80-2* was the highest homology with beech *FsPP2C2* (figure 1). Furthermore, *CsPP2C80s* had close genetic relationship with Arabidopsis class K of PP2C. The biological function of PP2C K class is still rarely reported.

In our previous study, the content of  $H_2O_2$  and superoxide anion dramatically accumulated after 5h and the expression of PP2C was induced by glucosaxose treatment in cucumber, however, the accumulation of ROS inhibited by DPI and DMTU pretreatment. With the question of why PP2C induced after ROS content increased, whether glucosaxose-induced resistance was related to ABA signaling and whether the PP2C was involved in ABA signaling pathway. We sought to further investigate the possible link among ROS accumulation, CsPP2C80s, ABA signaling and glucosaxose-induced resistance.

In this work, the endogenous ABA content increased obviously at 9 h after glucosaxose treatment, but DMTU and DPI pretreatment obviously inhibited the effect. ABA content increased slightly later than the accumulation of ROS. ROS accumulation and ABA content increased induced by glucosaxose. The relative expression levels of *CsPP2C80s* also induced by glucosaxose, reached the highest expression at 9 h, and DMTU, DPI pretreatment inhibited such exaltation in a certain extent. The changes of *CsPP2C80s* were consistent with ROS accumulation. Meanwhile, the relative expression of these allele genes of *PYL1* and *PYL2*, *SnRK2.1* and *SnRK2.2* also increased significantly after glucosaxose treatment, and DMTU, DPI pretreatment abolished this increase too. Endogenous ABA accumulation caused the changes of NADPH oxidase *Rbohs* gene expression at early stage, whereas DMTU or DPI

pretreatment restrained these changes. Thus, CsPP2C80s were involved in process of ROS produce and signal transduction induced by glucohexaose. We speculated that glucohexaose induce resistance partially due to ROS accumulation opening ABA signaling and CsPP2C80s might play a positive regulatory role in process of ABA combined with PYLs to activate SnRK2s and regulated NADPH oxidase to produce extracellular H<sub>2</sub>O<sub>2</sub> in cucumber. These results provided important clues of the mechanism of glucohexaose-induced resistance and lay the foundation of further evidence of reverse genetics to demonstrate the specific role of PP2C in cucumber.

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